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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent application

Appl'n. No. : 10/031,165
Filed : N/A
Applicant : Sheena M. Loosmore, et al.
Title : RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR
OUTER MEMBRANE PROTEIN OF MORAXELLA
Docket No. : 1038-1217 MIS:sd

May 13, 2002

BY COURIER

The Commissioner of Patents
and Trademarks,
Washington, D.C. 20231,
U.S.A.

VOLUNTARY AMENDMENT

Sir:

Please amend this application in the following manner:

In the disclosure:

Add the enclosed Sequence Listing following page 55 and immediately
preceding the claims.

REMARKS

The Sequence Listing is inserted into the specification hereby.

Respectfully submitted,
SIM & McBURNEY

Michael I. Stewart
Reg. No. 24,973

Enclosure(s)
Toronto, Ontario, Canada,
(416) 595-1155
FAX No. (416) 595-1163

SEQUENCE LISTING

<110> LOOSMORE, Sheena M.
SASAKI, Ken
YANG, Yan-Ping
KLEIN, Michel H.

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PROTEIN OF MORAXELLA

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 Gly Ser Gly Thr Asn Asn Ser Leu Val Thr Ala Glu His Leu Ala Ser
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 Tyr Leu Asn Glu Val Asn Arg Thr Ala Asp Ser Ala Leu Gln Ser Phe
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 1825 1830 1835 1840
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 1845 1850 1855
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Asp Gly Thr Ala Gly Thr Thr Thr Thr Ala Gly Ala Thr Gly Thr Val
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Lys Gly Phe Ala Gly Gln Thr Ala Val Gly Ala Val Ser Val Gly Ala
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gacccaaact caggttcatc atctaaccgc atctgcatca aagcaggcac ggtactggc 1980
ggtaaaggta ataacgatac cgaaaaactt gccactgggtg gtatacaagt gggcgtggat 2040
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aaccgccgag aagccattga cagaataaat gaacaaggta tccgcttctt ccatgtcaac 2220
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<210> 46

<211> 1044

<212> PRT

<213> Moraxella catarrhalis

<400> 46

Gly Thr Val Thr Phe Gly Ile Asn Thr Thr Ser Gly Leu Lys Ala Gly

1

5

10

15

Lys Ser Thr Leu Asn Asp Gly Gly Leu Ser Ile Lys Asn Pro Thr Gly
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 Ser Glu Gln Ile Gln Val Gly Ala Asp Gly Val Lys Phe Ala Lys Val
 35 40 45
 Asn Asn Asn Gly Val Val Gly Ala Gly Ile Asp Gly Thr Thr Arg Ile
 50 55 60
 Thr Arg Asp Glu Ile Gly Phe Thr Gly Thr Asn Gly Ser Leu Asp Lys
 65 70 75 80
 Ser Lys Pro His Leu Ser Lys Asp Gly Ile Asn Ala Gly Gly Lys Lys
 85 90 95
 Ile Thr Asn Ile Gln Ser Gly Glu Ile Ala Gln Asn Ser His Asp Ala
 100 105 110
 Val Thr Gly Gly Lys Ile Tyr Asp Leu Lys Thr Glu Leu Glu Asn Lys
 115 120 125
 Ile Ser Ser Thr Ala Lys Thr Ala Gln Asn Ser Leu His Glu Phe Ser
 130 135 140
 Val Ala Asp Glu Gln Gly Asn Asn Phe Thr Val Ser Asn Pro Tyr Ser
 145 150 155 160
 Ser Tyr Asp Thr Ser Lys Thr Ser Asp Val Ile Thr Phe Ala Gly Glu
 165 170 175
 Asn Gly Ile Thr Thr Lys Val Asn Lys Gly Val Val Arg Val Gly Ile
 180 185 190
 Asp Gln Thr Lys Gly Leu Thr Thr Pro Lys Leu Thr Val Gly Asn Asn
 195 200 205
 Asn Gly Lys Gly Ile Val Ile Asp Ser Gln Asn Gly Gln Asn Thr Ile
 210 215 220
 Thr Gly Leu Ser Asn Thr Leu Ala Asn Val Thr Asn Asp Lys Gly Ser
 225 230 235 240
 Val Arg Thr Thr Glu Gln Gly Asn Ile Ile Lys Asp Glu Asp Lys Thr
 245 250 255
 Arg Ala Ala Ser Ile Val Asp Val Leu Ser Ala Gly Phe Asn Leu Gln
 260 265 270
 Gly Asn Gly Glu Ala Val Asp Phe Val Ser Thr Tyr Asp Thr Val Asn
 275 280 285
 Phe Ala Asp Gly Asn Ala Thr Thr Ala Lys Val Thr Tyr Asp Asp Thr
 290 295 300
 Ser Lys Thr Ser Lys Val Val Tyr Asp Val Asn Val Asp Asp Thr Thr
 305 310 315 320
 Ile Glu Val Lys Asp Lys Lys Leu Gly Val Lys Thr Thr Thr Leu Thr
 325 330 335

Ser Thr Gly Thr Gly Ala Asn Lys Phe Ala Leu Ser Asn Gln Ala Thr
 340 345 350
 Gly Asp Ala Leu Val Lys Ala Ser Asp Ile Val Ala His Leu Asn Thr
 355 360 365
 Leu Ser Gly Asp Ile Gln Thr Ala Lys Gly Ala Ser Gln Ala Asn Asn
 370 375 380
 Ser Ala Gly Tyr Val Asp Ala Asp Gly Asn Lys Val Ile Tyr Asp Ser
 385 390 395 400
 Thr Asp Asn Lys Tyr Tyr Gln Ala Lys Asn Asp Gly Thr Val Asp Lys
 405 410 415
 Thr Lys Glu Val Ala Lys Asp Lys Leu Val Ala Gln Ala Gln Thr Pro
 420 425 430
 Asp Gly Thr Leu Ala Gln Met Asn Val Lys Ser Val Ile Asn Lys Glu
 435 440 445
 Gln Val Asn Asp Ala Asn Lys Lys Gln Gly Ile Asn Glu Asp Asn Ala
 450 455 460
 Phe Val Lys Gly Leu Glu Lys Ala Ala Ser Asp Asn Lys Thr Lys Asn
 465 470 475 480
 Ala Ala Val Thr Val Gly Asp Leu Asn Ala Val Ala Gln Thr Pro Leu
 485 490 495
 Thr Phe Ala Gly Asp Thr Gly Thr Thr Ala Lys Lys Leu Gly Glu Thr
 500 505 510
 Leu Thr Ile Lys Gly Gly Gln Thr Asp Thr Asn Lys Leu Thr Asp Asn
 515 520 525
 Asn Ile Gly Val Val Ala Gly Thr Asp Gly Phe Thr Val Lys Leu Ala
 530 535 540
 Lys Asp Leu Thr Asn Leu Asn Ser Val Asn Ala Gly Gly Thr Lys Ile
 545 550 555 560
 Asp Asp Lys Gly Val Ser Phe Val Asp Ser Ser Gly Gln Ala Lys Ala
 565 570 575
 Asn Thr Pro Val Leu Ser Ala Asn Gly Leu Asp Leu Gly Gly Lys Val
 580 585 590
 Ile Ser Asn Val Gly Lys Gly Thr Lys Asp Thr Asp Ala Ala Asn Val
 595 600 605
 Gln Gln Leu Asn Glu Val Arg Asn Leu Leu Gly Leu Gly Asn Ala Gly
 610 615 620
 Asn Asp Asn Ala Asp Gly Asn Gln Val Asn Ile Ala Asp Ile Lys Lys
 625 630 635 640

Asp Pro Asn Ser Gly Ser Ser Ser Asn Arg Thr Val Ile Lys Ala Gly
 645 650 655
 Thr Val Leu Gly Gly Lys Gly Asn Asn Asp Thr Glu Lys Leu Ala Thr
 660 665 670
 Gly Gly Ile Gln Val Gly Val Asp Lys Asp Gly Asn Ala Asn Gly Asp
 675 680 685
 Leu Ser Asn Val Trp Val Lys Thr Gln Lys Asp Gly Ser Lys Lys Ala
 690 695 700
 Leu Leu Ala Thr Tyr Asn Ala Ala Gly Gln Thr Asn Tyr Leu Thr Asn
 705 710 715 720
 Asn Pro Ala Glu Ala Ile Asp Arg Ile Asn Glu Gln Gly Ile Arg Phe
 725 730 735
 Phe His Val Asn Asp Gly Asn Gln Glu Pro Val Val Gln Gly Arg Asn
 740 745 750
 Gly Ile Asp Ser Ser Ala Ser Gly Lys His Ser Val Ala Ile Gly Phe
 755 760 765
 Gln Ala Lys Ala Asp Gly Glu Ala Ala Val Ala Ile Gly Arg Gln Thr
 770 775 780
 Gln Ala Gly Asn Gln Ser Ile Ala Ile Gly Asp Asn Ala Gln Ala Thr
 785 790 795 800
 Gly Asp Gln Ser Ile Ala Ile Gly Thr Gly Asn Val Val Ala Gly Lys
 805 810 815
 His Ser Gly Ala Ile Gly Asp Pro Ser Thr Val Lys Ala Asp Asn Ser
 820 825 830
 Tyr Ser Val Gly Asn Asn Asn Gln Phe Thr Asp Ala Thr Gln Thr Asp
 835 840 845
 Val Phe Gly Val Gly Asn Asn Ile Thr Val Thr Glu Ser Asn Ser Val
 850 855 860
 Ala Leu Gly Ser Asn Ser Ala Ile Ser Ala Gly Thr His Ala Gly Thr
 865 870 875 880
 Gln Ala Lys Lys Ser Asp Gly Thr Ala Gly Thr Thr Thr Thr Ala Gly
 885 890 895
 Ala Thr Gly Thr Val Lys Gly Phe Ala Gly Gln Thr Ala Val Gly Ala
 900 905 910
 Val Ser Val Gly Ala Ser Gly Ala Glu Arg Arg Ile Gln Asn Val Ala
 915 920 925
 Ala Gly Glu Val Ser Ala Thr Ser Thr Asp Ala Val Asn Gly Ser Gln
 930 935 940
 Leu Tyr Lys Ala Thr Gln Ser Ile Ala Asn Ala Thr Asn Glu Leu Asp
 945 950 955 960

His Arg Ile His Gln Asn Glu Asn Lys Ala Asn Ala Gly Ile Ser Ser
965 970 975

Ala Met Ala Met Ala Ser Met Pro Gln Ala Tyr Ile Pro Gly Arg Ser
980 985 990

Met Val Thr Gly Gly Ile Ala Thr His Asn Gly Gln Gly Ala Val Ala
995 1000 1005

Val Gly Leu Ser Lys Leu Ser Asp Asn Gly Gln Trp Val Phe Lys Ile
1010 1015 1020

Asn Gly Ser Ala Asp Thr Gln Gly His Val Gly Ala Ala Val Gly Ala
1025 1030 1035 1040

Gly Phe His Phe

<210> 47

<211> 2448

<212> DNA

<213> Moraxella catarrhalis

<400> 47

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gatggcggtga	agtttgccaa	ggttaataat	aatgggtgtg	taggtgctgg	cattgatggc	180
acaactcgca	ttaccagaga	tgaatttggc	tttactggga	ctaattggctc	acttgataaa	240
agcaaacccc	acctaagcaa	agacggcatt	aacgcagggtg	gtaaaaagat	taccaacatt	300
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gccaaagaca	aactggctgc	ccaagcccaa	acccagatg	gcacattggc	tcaaatagat	1320
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agcaaaaaag ccctgctcgc cacttataac gccgcaggtc agaccaacta tttgaccaac 2160
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```

<210> 48

<211> 816

<212> PRT

<213> *Moraxella catarrhalis*

<400> 48

```

Gly Thr Val Thr Phe Gly Ile Asn Thr Thr Ser Gly Leu Lys Ala Gly
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```

```

Lys Ser Thr Leu Asn Asp Gly Gly Leu Ser Ile Lys Asn Pro Thr Gly
      20             25             30

```

```

Ser Glu Gln Ile Gln Val Gly Ala Asp Gly Val Lys Phe Ala Lys Val
 35             40             45

```

```

Asn Asn Asn Gly Val Val Gly Ala Gly Ile Asp Gly Thr Thr Arg Ile
 50             55             60

```

```

Thr Arg Asp Glu Ile Gly Phe Thr Gly Thr Asn Gly Ser Leu Asp Lys
 65             70             75             80

```

```

Ser Lys Pro His Leu Ser Lys Asp Gly Ile Asn Ala Gly Gly Lys Lys
      85             90             95

```

```

Ile Thr Asn Ile Gln Ser Gly Glu Ile Ala Gln Asn Ser His Asp Ala
 100            105            110

```

```

Val Thr Gly Gly Lys Ile Tyr Asp Leu Lys Thr Glu Leu Glu Asn Lys
 115            120            125

```

```

Ile Ser Ser Thr Ala Lys Thr Ala Gln Asn Ser Leu His Glu Phe Ser
 130            135            140

```

```

Val Ala Asp Glu Gln Gly Asn Asn Phe Thr Val Ser Asn Pro Tyr Ser
 145            150            155            160

```

```

Ser Tyr Asp Thr Ser Lys Thr Ser Asp Val Ile Thr Phe Ala Gly Glu
 165            170            175

```

```

Asn Gly Ile Thr Lys Val Asn Lys Gly Val Val Arg Val Gly Ile
 180            185            190

```

```

Asp Gln Thr Lys Gly Leu Thr Thr Pro Lys Leu Thr Val Gly Asn Asn
 195            200            205

```

```

Asn Gly Lys Gly Ile Val Ile Asp Ser Gln Asn Gly Gln Asn Thr Ile
 210            215            220

```

Thr Gly Leu Ser Asn Thr Leu Ala Asn Val Thr Asn Asp Lys Gly Ser
 225 230 235 240
 Val Arg Thr Thr Glu Gln Gly Asn Ile Ile Lys Asp Glu Asp Lys Thr
 245 250 255
 Arg Ala Ala Ser Ile Val Asp Val Leu Ser Ala Gly Phe Asn Leu Gln
 260 265 270
 Gly Asn Gly Glu Ala Val Asp Phe Val Ser Thr Tyr Asp Thr Val Asn
 275 280 285
 Phe Ala Asp Gly Asn Ala Thr Thr Ala Lys Val Thr Tyr Asp Asp Thr
 290 295 300
 Ser Lys Thr Ser Lys Val Val Tyr Asp Val Asn Val Asp Asp Thr Thr
 305 310 315 320
 Ile Glu Val Lys Asp Lys Lys Leu Gly Val Lys Thr Thr Thr Leu Thr
 325 330 335
 Ser Thr Gly Thr Gly Ala Asn Lys Phe Ala Leu Ser Asn Gln Ala Thr
 340 345 350
 Gly Asp Ala Leu Val Lys Ala Ser Asp Ile Val Ala His Leu Asn Thr
 355 360 365
 Leu Ser Gly Asp Ile Gln Thr Ala Lys Gly Ala Ser Gln Ala Asn Asn
 370 375 380
 Ser Ala Gly Tyr Val Asp Ala Asp Gly Asn Lys Val Ile Tyr Asp Ser
 385 390 395 400
 Thr Asp Asn Lys Tyr Tyr Gln Ala Lys Asn Asp Gly Thr Val Asp Lys
 405 410 415
 Thr Lys Glu Val Ala Lys Asp Lys Leu Val Ala Gln Ala Gln Thr Pro
 420 425 430
 Asp Gly Thr Leu Ala Gln Met Asn Val Lys Ser Val Ile Asn Lys Glu
 435 440 445
 Gln Val Asn Asp Ala Asn Lys Lys Gln Gly Ile Asn Glu Asp Asn Ala
 450 455 460
 Phe Val Lys Gly Leu Glu Lys Ala Ala Ser Asp Asn Lys Thr Lys Asn
 465 470 475 480
 Ala Ala Val Thr Val Gly Asp Leu Asn Ala Val Ala Gln Thr Pro Leu
 485 490 495
 Thr Phe Ala Gly Asp Thr Gly Thr Thr Ala Lys Lys Leu Gly Glu Thr
 500 505 510
 Leu Thr Ile Lys Gly Gly Gln Thr Asp Thr Asn Lys Leu Thr Asp Asn
 515 520 525
 Asn Ile Gly Val Val Ala Gly Thr Asp Gly Phe Thr Val Lys Leu Ala
 530 535 540

Lys Asp Leu Thr Asn Leu Asn Ser Val Asn Ala Gly Gly Thr Lys Ile
 545 550 555 560
 Asp Asp Lys Gly Val Ser Phe Val Asp Ser Ser Gly Gln Ala Lys Ala
 565 570 575
 Asn Thr Pro Val Leu Ser Ala Asn Gly Leu Asp Leu Gly Gly Lys Val
 580 585 590
 Ile Ser Asn Val Gly Lys Gly Thr Lys Asp Thr Asp Ala Ala Asn Val
 595 600 605
 Gln Gln Leu Asn Glu Val Arg Asn Leu Leu Gly Leu Gly Asn Ala Gly
 610 615 620
 Asn Asp Asn Ala Asp Gly Asn Gln Val Asn Ile Ala Asp Ile Lys Lys
 625 630 635 640
 Asp Pro Asn Ser Gly Ser Ser Ser Asn Arg Thr Val Ile Lys Ala Gly
 645 650 655
 Thr Val Leu Gly Gly Lys Gly Asn Asn Asp Thr Glu Lys Leu Ala Thr
 660 665 670
 Gly Gly Ile Gln Val Gly Val Asp Lys Asp Gly Asn Ala Asn Gly Asp
 675 680 685
 Leu Ser Asn Val Trp Val Lys Thr Gln Lys Asp Gly Ser Lys Lys Ala
 690 695 700
 Leu Leu Ala Thr Tyr Asn Ala Ala Gly Gln Thr Asn Tyr Leu Thr Asn
 705 710 715 720
 Asn Pro Ala Glu Ala Ile Asp Arg Ile Asn Glu Gln Gly Ile Arg Phe
 725 730 735
 Phe His Val Asn Asp Gly Asn Gln Glu Pro Val Val Gln Gly Arg Asn
 740 745 750
 Gly Ile Asp Ser Ser Ala Ser Gly Lys His Ser Val Ala Ile Gly Phe
 755 760 765
 Gln Ala Lys Ala Asp Gly Glu Ala Ala Val Ala Ile Gly Arg Gln Thr
 770 775 780
 Gln Ala Gly Asn Gln Ser Ile Ala Ile Gly Asp Asn Ala Gln Ala Thr
 785 790 795 800
 Gly Asp Gln Ser Ile Ala Ile Gly Thr Gly Asn Val Val Ala Gly Lys
 805 810 815